

COMMENT

Other_ESTs: EST06373
Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: mdadams@tigr.org
Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

```
1. .357
/organism="Homo sapiens"
/db_xref="ATCC (inhost):85007"
/db_xref="taxon:9606"
/clone="HTBBE91"
/clone_lib="Infant Brain, Bent
```

BASE COUNT

ORIGIN

90 a 107 c 96 g 61 t 3 others

```

Query Match      8.9%;  Score 248.6;  DB 145;  Length 357;
Best Local Similarity 83.1%;  Pred. No. 3.7e-47;
Matches 281;  Conservative 0;  Mismatches 57;  Indels 0;  Gaps 0;

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| | | | |
|----|------|---|------|
| Qy | 897 | atctcacctgtggggtgtgcaccctggagctggggagcaccagggtcctgctggaccacc | 956 |
| | | | |
| Db | 1 | ACCTCACCTGTGGGTTCTGTGCCCTGGAGCTAGGGAGCACCAGGTGCTACTGGACCACC | 60 |
| | | | |
| Qy | 957 | tcaagtctcacgcggaagaaaaaggccaaccaggccacccaggggagaagaaataccagtgcg | 1016 |
| | | | |
| Db | 61 | TCANAGCCCATGCGBAAGAGAAGCCCCCTAGCGGAACCAAGGAAAAGAAGCACCAGTGCG | 120 |
| | | | |
| Qy | 1017 | accactgtgatagatgcttctacacctcgaaagatgtgctgcgccacctgggtggtccaca | 1076 |
| | | | |
| Db | 121 | ACCACTGTGAAAGATGCTTCTACACCCGGAAGGATGTGCGACGCCACCTGGTGGTCCACA | 180 |
| | | | |
| Qy | 1077 | caggatgcaaggacttcctgtgtcagttctgtgccagagatttgggcgcaaagaccacc | 1136 |
| | | | |
| Db | 181 | CAGGATGCAAGGACTTCCTGTGCCAGTTCTGTGCCAGAGATTGGGCGCAAAGGTTACC | 240 |
| | | | |
| Qy | 1137 | tcactcgtcacaccaagaagaccactcccaggagctgatgcaagagaatatgcaggcgag | 1196 |
| | | | |
| Db | 241 | TCACCCGGCATACCAAGAAGACCCACTCACAGGAGCTGATGAAAGAGAGCTTGCAGACCG | 300 |
| | | | |
| | | | |
| Qy | 1197 | gagattaccagagcaatttccaactcattgcgccttca | 1234 |
| | | | |
| Db | 301 | GAGACCTTCTGAGCACCTTNACACCATCTCGNCTTCA | 338 |

RESULT 13

F11702

LOCUS

DEFINITION

F11702 340 bp mRNA EST 12-MAR-1995
HSC30E051 normalized infant brain cDNA Homo sapiens cDNA clone
c-30e05, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

F11702
F11702.1 GI:706008
EST.
human.

REFERENCE

AUTHORS

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 340)
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes,
M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F.,
Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
Sebastiani-Kabaktchis, C. and Tessier, A.

TITLE

1000

JOURNAL

MEDLI

Sebastiani-Kabaktchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800

95277534
Contact: Genethon
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Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y2c-2sh08
Seq primer: (-21)M13 universal.

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1. Location/Qualifiers
1. .301
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-2sh08"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site 2: NotI; sex:Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue type=total brain
; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

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Query Match 8.2%; Score 228.4; DB 140; Length 301;
Best Local Similarity 84.3%; Pred. No. 1.7e-42;
Matches 253; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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F08789          LOCUS          290 bp      mRNA          EST          20-FEB-1995
DEFINITION      HSC2AH041 normalized infant brain cDNA Homo sapiens cDNA clone
                  c-2ah04, mRNA sequence.
ACCESSION       F08789
VERSION         F08789.1  GI:673259
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 290)
AUTHORS         Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
                  ,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
                  Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
                  Sebastiani-Kabaktchis,C. and Tessier,A.
TITLE           IMAGE: molecular integration of the analysis of the human genome

```

and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr

FEATURES
source

```

Location/Qualifiers
1. .290
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-2ah04"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII;
Site 2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain
; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

```

BASE COUNT
ORIGIN

Bento Soares, P.N.A.S in press
75 a 81 c 85 g 46 t 3 others

```

Query Match      8.1%;  Score 226.2;  DB 140;  Length 290;
Best Local Similarity 85.9%;  Pred. No. 5.4e-42;
Matches 249;  Conservative 0;  Mismatches 41;  Indels 0;  Gaps 0;

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| | | | | | | |
|----|------|------------------------|---------|--|--------------|--|
| | | | MATCHES | 2497 | CONSOLIDATED | |
| Qy | 893 | ggcgatctcacctgtg | | gggggtgtgcaccctggagctggggagcaccgaggtcctgctggac | 952 | |
| Db | 1 | GGGGACCTCACCTGTG | | GGCGTCTGCCCTGGAGCTAGGGAGCNCNGAGGTGCTACTGGAC | 60 | |
| Qy | 953 | cacctcaagtctcacgcgaaga | | aaaaggccaaccaggcaccagggagaagaaataccag | 1012 | |
| Db | 61 | CANTTCAAAGCCCATGC | | GGAAGAAGCCCCCTAGCGGANCCAAGGAAAAGAAGCACCAG | 120 | |
| Qy | 1013 | tgcgaccactgtgatagatg | | cttctacacccgaaagatgtg | 1072 | |
| Db | 121 | TGCGACCACTGTGAAAGAT | | GCTTCTACACCCGGAAGGATGTGCGACGCCACCTGGTG | 180 | |
| Qy | 1073 | cacacaggatgcaaggacttc | | ctgtgtcagttctgtgccagagatttg | 1132 | |
| Db | 181 | CACACAGGATGCAAGGACTT | | CCTGTGCCAGTTCTGTGCCAGAGATTGGGCGCAAGGTT | 240 | |
| Qy | 1133 | cacctcactcgtcacaccaaga | | agaccccactcccaggagctgatgcaaga | 1182 | |
| Db | 241 | CACCTCACCCGGCATACCA | | AAGAAGACCCACTCACAGGAGCTGATGAAAGA | 290 | |

| | | | |
|----|------|---|------|
| Db | 993 | CCAGGGAGAAGAAATACCACTGCGACCACTGTGATAGATGCTTCTACACCCGGAAAGATG | 1052 |
| Qy | 1314 | tgcgacgccacctggtggtccacacaggatgcaaggacttcctgtgccagttctgtgccc | 1373 |
| Db | 1053 | TGCGTCGCCACCTGGTGGTCCACACAGGATGCAAGGACTTCTGTGTCAGTTCTGTGCCC | 1112 |
| Qy | 1374 | agagatttgggcgcaaggatcacctcaccggcgcataccaagaagacccactcacaggagc | 1433 |
| Db | 1113 | AGAGATTGCGCGCAAAGACCACCTCACTCGTCACACCAAGAAGACCCACTCCCAGGAGC | 1172 |
| Qy | 1434 | tgatgaaagagagccttgagaccggagaccttctgagcaccttccacaccatctcgctt | 1493 |
| Db | 1173 | TGATGCAAGAGAATATGCAGGCAGGAGATTACCAGAGCAATTTCCAACCTCATTGCGCCTT | 1232 |
| Qy | 1494 | ca-----ttccaactgaaggctgctgccttgccctcctttccctttaggagccttctgccc | 1547 |
| Db | 1233 | CAACTTCGTTCCAGATAAAGGTTGATCCCATGCCTCCTTTCCAGCTAGGAGCGGCTCCCCG | 1292 |
| Qy | 1548 | agaacgggcttgcaagtagccttgccagctgaggtccatagcctcaccctcagtcccccag | 1607 |
| Db | 1293 | AGAACGGGCTTGATGGTGGCTTGCCACCCGAGGTTTCATGGTCTAGTGCTTGCTGCCCCAG | 1352 |
| Qy | 1608 | aacaagccgcccagcctatgcagccgctg | 1636 |
| Db | 1353 | AAGAAGCTCCCCAACCCATGCCGCCCTTG | 1381 |

| | | | |
|----|-----|---|-----|
| Qy | 1 | MATFPCQLCGKTFLTLEKFTIHNYSHSRERPYKCVQPDGKAFVSRYKLMRHMATHSPQK | 60 |
| Db | 1 | MATFPCQLCGKTFLTLEKFTIHNYSHSRERPYKCVQPDGKAFVSRYKLMRHMATHSPQK | 60 |
| Qy | 61 | SHQCAHCEKTFNRKDHLKNHLQTHDPNKMAFGCEECGKKYNTMLGYKRHLALHAASSGDL | 120 |
| Db | 61 | SHQCAHCEKTFNRKDHLKNHFQTHDPNKMAFGCEECGKKYNTMLGYKRHLALHAASSGDL | 120 |
| Qy | 121 | TCGVCALELGSTEVLLDHLKAHAEEKPPSGTKEKKHQCDHCERC FYTRKDVRRHLVVHTG | 180 |
| Db | 121 | TCGVCALELGSTEVLLDHLKAHAEEKPPSGTKEKKHQCDHCERC FYTRKDVRRHLVVHTG | 180 |
| Qy | 181 | CKDFLCQFCAQRFGRKDHLTRHTKKTHSQELMKESLQTGDLLSTFHTISPSFQLKAAALP | 240 |
| Db | 181 | CKDFLCQFCAQRFGRKDHLTRHTKKTHSQELMKESLQTGDLLSTFHTISPSFQLKAAALP | 240 |
| Qy | 241 | PFPLGASAQNGLASSLPAEVHSLTSPPEQAAQPMQPLPESLASLHPSVSPGSPPPPLPN | 300 |
| Db | 241 | PFPLGASAQNGLASSLPAEVHSLTSPPEQAAQPMQPLPESLASLHPSVSPGSPPPPLPN | 300 |
| Qy | 301 | HKYNTTSTSYSPLASLPLKADTKGFCNISLFEDLPLQEPQSPQKLNPGFDLAKGNAGKVN | 360 |
| Db | 301 | HKYNTTSTSYSPLASLPLKADTKGFCNISLFEDLPLQEPQSPQKLNPGFDLAKGNAGKVN | 360 |
| Qy | 361 | LPKELPADAVNLTIPASLDLSPLLGFWQLPPPATQNTFGNSTLALGPGESLPHRLSCLGQ | 420 |
| Db | 361 | LPKELPADAVNLTIPASLDLSPLLGFWQLPPPATQNTFGNSTLALGPGESLPHRLSCLGQ | 420 |
| Qy | 421 | QQQEPPLAMGTVSLGQLPLPPIPHVFSAGTGSAILPHFHHAFR | 463 |
| Db | 421 | QQQEPPLAMGTVSLGQLPLPPIPHVFSAGTGSAILPHFHHAFR | 463 |

RESULT 5
P70616
ID P70616 PRELIMINARY; PRT; 583 AA.
AC P70616;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE LOT1.
GN LOT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=97294608; PubMed=9150364;
RA Abdollahi A., Roberts D., Godwin A.K., Schultz D.C., Sonoda G.,
RA Testa J.R., Hamilton T.C.;
RT "Identification of a zinc-finger gene at 6q25: a chromosomal region
RT implicated in development of many solid tumors.";
RL Oncogene 14:1973-1979(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=97301600; PubMed=9158001;
RA Abdollahi A., Godwin A.K., Miller P.D., Getts L.A., Schultz D.C.,
RA Taguchi T., Testa J.R., Hamilton T.C.;
RT "Identification of a gene containing zinc-finger motifs based on lost
RT expression in malignantly transformed rat ovarian surface epithelial
RT cells.";
RL Cancer Res. 57:2029-2034(1997).
DR EMBL; U72620; AAB67042.1; -.
DR HSSP; P03001; 1TF3.
DR INTERPRO; IPR000822; -.
DR PFAM; PF00096; zf-C2H2; 7.
DR PRINTS; PR00048; ZINCFINGER.
DR PROSITE; PS00028; ZINC FINGER C2H2; 7.
KW Zinc-finger; Metal-binding; DNA-binding.
SQ SEQUENCE 583 AA; 65960 MW; 8501071AADFB3F4B CRC64;

Query Match 70.1%; Score 1763; DB 11; Length 583;
Best Local Similarity 56.6%; Pred. No. 1.6e-135;
Matches 330; Conservative 49; Mismatches 84; Indels 120; Gaps 4;

QY 1 MATFPCQLCGKTFLTLEKFTIHNYSHSRERPYKCVQPCGKAFVSRYSKLMRHMATHSPQK 60
Db 1 MAPFRCQKCGKSFLTLEKFTIHNYSHTRERPFKCSKTECGKAFVSKYKLMRHMATHSPQK 60
QY 61 SHQCAHCEKTFNRKDHLKKNHLQTHDPNKMAFGCEECKKYNMGLGYKRHLALHAASSGDL 120
Db 61 THQCTHCEKTFNRKDHLKKNHLQTHDPNKMIYACEDCGKKYHTMGLGYKRHMALHSASSGDL 120
QY 121 TCGVCALELGGSTEVLDDHLKAHAEEKPPSGTKEKKHQCDHCERCIFYTRKDVRRHLVVHTG 180
Db 121 TCGVCTLELGGSTEVLDDHLKSHAEEKAHAPREKKHQCDHCERCIFYTRKDVRRHLVVHTG 180
QY 181 CKDFLCQFCAQRFGRKDHLTRHTKKTHSQELMKESLQTDLLSTFHTISPSFQKAAALP 240
Db 181 CKDFLCQFCAQRFGRKDHLTRHTKKTHSQELMQESLQAGEYQGGYQPIAPPFQIKADPMP 240
QY 241 PFPLGASAQNGGLASSLP AEVHSLTSLPPEQAAQ-----PMQPLPESLASLHPSVSPGSP 294
Db 241 PFQLEMPPEGLDGGGLPPEIHGLVLASPEEVPQPMLSMPMPQPMPEQPFTLHPGVVPSSP 300
QY 295 PP-PLPNHKYNTTSTSYSPLASLPLKADTKGFCNISLFEDLPLQEPQSPQKLNPGFDIAK 353
Db 301 PPIILQEHKYSVPVTSFAPFVSMMPKADLKGFCNMGLFEEFPLQECQSPVKFSQCFEMAK 360
QY 354 GNAGKVNLPKELPADAVNLTIPASLDLSPLLGFQWQLPPPATQNTFGNSTLALGPGESLPH 413
Db 361 EGFGKVTLPKELLVDAVNIAIPGSLEISLLGFQWQLPPPPQNGFMNGTIPVGAGEPLPH 420

[illegible]

US-09-254-870A-2

W48761

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Query Match

Best Local Similarity

Matches 310; Conservative

Qy

Db

Qy

| | | | |
|----|-----|---|-----|
| Db | 61 | shqcahcektfnrkdhlknhlqthdnpkmafgceecgkkyntmlgykrhlalhaassgd1 | 120 |
| Qy | 121 | TCGVCTLELGSTEVLDDHLKSHAEKANQAPREKKYQCDHCDRCFYTRKDVRRHLVVHTG | 180 |
| Db | 121 | tcgvcalelgstevlldhlkahaeeekppsgtkekkhqcdhcercfytrkdvrhlvvhtg | 180 |
| Qy | 181 | CKDFLCQFCAQRFGRKDHLTRHTKKTHSQELMQENMQAGDYQSNFQLIAPSTSFQIKVDP | 240 |
| Db | 181 | ckdfllcqfcaqrfgrkdhltrhtkkthsqelmkeslgtgdllstfhtisp--sfqlkaa | 238 |
| Qy | 241 | MPPFQLGAAPENGLDGLPPEVHGLVLAAPEEAPQPMPPLEPLEPLEPLEPMQSLEP | 300 |
| Db | 239 | lppfplgasagnglasslpaevhsltlspeqaaqpmqpl----- | 278 |
| Qy | 301 | LQPLEPMQPLEPMQPLEPMQPLEPLEPLEPMQPLEPMQPLEPMQMLPMQPMQPMQPMQ | 360 |
| Db | 279 | ----- | 278 |
| Qy | 361 | MLPMQPMMLPMQPMQPMQPMQPMPEPSFTLHPGVVPTSPPPPIILQEHKYNPVPTSYPFVG | 420 |
| Db | 279 | -----peslaslhpsvsgsppp-plpnhkynttstsysplas | 315 |
| Qy | 421 | MPVKADGKAFCNVGFFEEFPLQEPQAPLKFNPCFEMPMEGFGKVTLSKELLVDAVNIAIP | 480 |
| Db | 316 | lplkadtkgfcnislfedlplqepqspqklnpgfdlakgnagkvnlpkelpadavnltp | 375 |
| Qy | 481 | ASLEISSLLGFWQLPPPTPQNGFVNSTIPVGPGEPLPHRITCLA-QQQPPPLP----- | 532 |
| Db | 376 | asldlspllgfwqlpppatqntfgnstlalgpgeslphrlsclgqqqqepplamgtvslg | 435 |
| Qy | 533 | --PPPPLP | 538 |
| Db | 436 | qlplppip | 443 |